Claims

What is claimed is:

1. An isolated polypeptide having glucose isomerase activity, selected from the group consisting of:

(a) a polypeptide having an amino acid sequence which has at least 95% identity with amino acids for the mature polypeptide of SEQ ID NO:2;

(b) a variant of the polypeptide having an amino acid sequence of SEQ ID NO:2 comprising a substitution, deletion, and/or insertion of one or more amino acids;

(c) a fragment of (a) that has glucose isomerase activity; and

(d) a polypeptide having a pH optimum in the range of 5.7 to 6.3 at 60 °C, a pH optimum in the range of 6.1 to 6.7 at 90 °C and a temperature optimum of above 90 °C.

2. The polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:2.

3. The polypeptide of claim 1, which has a pH optimum in the range of 5.9 to 6.1 at 60 °C.

4. The polypeptide of claim 1, which has a pH optimum in the range of 6.3 to 6.5 at 90 °C.

5. The polypeptide of claim 1, which has a pH optimum of about 6 at 60 °C, a pH optimum of about 6.4 at 90 °C and a temperature optimum of 90 to 100 °C.

6. The polypeptide of claim 1, which has a specific activity on fructose substrate of at least 15 unitF/mg.

7. The polypeptide of claim 1, which is encoded by the nucleic acid sequence contained in plasmid pBSK1 or plasmid pBSK2.

8. The polypeptide of claim 1 being derived from the strain *Streptomyces* sp. SK (GI SK).

9. The strain *Streptomyces sp. SK* expressing genes encoding a polypeptide of claim 1.

10. A glucose isomerase GI in which a residue other than alanine at a position equivalent to position 100, 102 and/or 109 of GI SK has/have been replaced by alanine.

11. The glucose isomerase of claim 10, wherein the corresponding naturally occurring GI is derived from a microorganism of the order *Actinomycetales*.

12. The glucose isomerase of claim 11, wherein the corresponding naturally occurring GI is derived from a microorganism of *Streptomyces*.

13. An isolated nucleic acid sequence comprising a nucleic acid sequence which encodes the polypeptide of claim 1.

14. An isolated nucleic acid sequence comprising a nucleic acid sequence having at least one mutation in the mature polypeptide coding sequence of SEQ ID NO:1, in which the mutant nucleic acid sequence encodes a polypeptide consisting of amino acids of SEQ ID NO:2.

15. A nucleic acid construct comprising the nucleic acid sequence of claim 13 operably linked to one or more control sequences that direct the production of the polypeptide in a suitable expression host.

16. A recombinant expression vector comprising the nucleic acid construct of claim 15.

17. A recombinant host cell comprising the nucleic acid construct of claim 15.

18. A method for producing a mutant nucleic acid sequence, comprising: (a) introducing

at least one mutation into the mature polypeptide coding sequence of SEQ ID NO:1; and (b) recovering the mutant nucleic acid sequence.

19. A mutant nucleic acid sequence produced by the method of claim 18.

20. A method for producing a polypeptide, comprising: (a) cultivating a strain comprising the mutant nucleic acid sequence of claim 19 encoding the polypeptide under conditions suitable for production of the polypeptide; and (b) recovering the polypeptide from the strain or supernatant, or recovering the strain containing the polypeptide.

21. A method for producing the polypeptide of claim 1 comprising: (a) cultivating a strain to produce a supernatant comprising the polypeptide; and (b) recovering the polypeptide from the strain or supernatant, or recovering the strain containing the polypeptide.

22. A method for producing the polypeptide of claim 1 comprising: (a) cultivating a host cell comprising a nucleic acid construct comprising a nucleic acid sequence encoding the polypeptide under conditions suitable for production of the polypeptide; and (b) recovering the polypeptide from the host cell or supernatant, or recovering the host cell containing the polypeptide.